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## FOR THE RECORD

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# Haplotype Distributions of Four New Y-STRs: DYS588, DYS622, DYS623 and DYS630 in a Chinese Population

**POPULATION:** Han in eastern China

**KEYWORDS:** forensic science, DNA typing, Y-chromosome, short tandem repeats, eastern Chinese Han population, population genetics, DYS588, DYS622, DYS623, DYS630

EDTA-blood specimens for this study were drawn randomly from 86 Han-ethnic male individuals representing various geographical counties in eastern China, under their consent. Ethnic origin was determined by self-declaration. Additionally, 20 female EDTA-blood specimens were collected from the blood banks in Suzhou, Jiangsu province, China. Genomic DNA was extracted from whole blood samples using the chelex extraction procedure (1).

The primers of the four Y-STR loci DYS588, DYS622, DYS623 and DYS630 were synthesized by Life Technologies Inc. according to the GDB primer sequence which were shown in Table 1. PCR was performed using 1–30 ng of genomic DNA in a 37.5 μL final reaction volume. In the PCR protocol, the DNA was initially denatured at 94°C for 5 min. This was followed with 94°C for 50 s, 61°C for 50 s and 72°C for 40 s. A total of 32 cycles was carried out in an Eppendorf Mastercycler gradient system. The PCR products were analyzed by non-denaturing polyacrylamide gel electrophoresis and visualized by silver staining (2). PCR products were eluted from the gels and purified before sequencing. An example of each allele was sequenced on an ABI 377 automated sequencer using Dye Terminator Cycle Sequencing Kit (PE Applied Biosystems). The alleles were also cloned using the pGEM-T Easy Vector System I (Promega Corporation) according to the manufacturer's instruction. The DNA clones were sequenced with the ABI 377 automated sequencer to verify the allele sequences.

During the genotyping procedure, no PCR products were found for all the 20 female specimens at the four Y-STR loci, which indicated the male specificity of the four Y-chromosome STR loci we studied. Allele determination were carried out by comparison with a sequenced human allele ladder, which was made in-house and contained all the alleles found in this study, Allele designation was established following the recommendations of the DNA commission of the ISFH (3). The allele frequencies were calculated by counting method, The gene diversity, haplotype diversity as well as the stand error (S.E.) for the four Y-STRs were calculated according to Hou's method (4).

The four loci analyzed consisted of three tetranucleotide repeat and one pentanucleotide repeat which was shown in Table 1. Table 2 shows the allele frequencies and gene diversity values for all four Y-specific STR loci in a Chinese population. Five alleles at DYS588, six alleles at DYS622, four alleles at DYS623 and seven alleles at DYS630 were observed in our population sample. The distribution of haplotypes in the Chinese Han population is shown in Table 3. A total of 48 different haplotypes was observed in 86 males. The haplotype diversity for all four Y-specific STR loci in Chinese population was calculated to be 97.7% and the S.E. was calculated to be 0.38%.

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TABLE 1—*Locus designations and PCR primers for the four Y-STRs.*

| Locus | GenBank accession ID | Motif | Primer | Sequences |
|---|---|---|---|---|
| DYS588 | GDB:11503994 | TTGCA | Y5C23f | 5′ GAATGCAGAACCCTCAAGGA |
| | | | Y5C23r | 5′ AGCCTGGGTGACAGAAACAC |
| DYS622 | GDB:11510443 | AAAG | Y4C118f | 5′ TCCAGCCTCGGTGATAAGAG |
| | | | Y4C118r | 5′ GGCTGAAGTGGGTTGTGTTA |
| DYS623 | GDB:11510445 | GATA | Y4C119f | 5′ GGGAAAAGCGCCTTGTAACT |
| | | | Y4C119r | 5′ GGCTGGTTAGTCTCATGCTG |
| DYS630 | GDB:11510465 | GAAA | Y4C55f | 5′ GCCTTTGGACAGAGCAAGAC |
| | | | Y4C55r | 5′ AGCCATGGAAAGCTGTGAGT |

TABLE 2—*Allele frequencies of four Y-STR loci in a Chinese population.*

| Locus | Allele | Frequency | Gene Diversity | Standard Error |
|---|---|---|---|---|
| DYS588 | 13 | 0.151 | 0.373 | 0.042 |
| | 14 | 0.779 | | |
| | 15 | 0.023 | | |
| | 16 | 0.023 | | |
| | 18 | 0.023 | | |
| DYS622 | 16 | 0.023 | 0.785 | 0.009 |
| | 17 | 0.267 | | |
| | 18 | 0.267 | | |
| | 19 | 0.186 | | |
| | 20 | 0.209 | | |
| | 21 | 0.047 | | |
| DYS623 | 12 | 0.012 | 0.473 | 0.038 |
| | 13 | 0.105 | | |
| | 14 | 0.698 | | |
| | 15 | 0.186 | | |
| DYS630 | 21 | 0.012 | 0.797 | 0.012 |
| | 22 | 0.116 | | |
| | 23 | 0.233 | | |
| | 24 | 0.302 | | |
| | 25 | 0.198 | | |
| | 26 | 0.116 | | |
| | 27 | 0.023 | | |

The complete data can be obtained from the authors on request to: yuzhengao@suda.edu.cn

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TABLE 3—*Y-specific STR haplotype in a Chinese population.*

| Haplotype | Locus | | | | Number | Haplotype Frequency |
|---|---|---|---|---|---|---|
| | DYS588 | DYS622 | DYS623 | DYS630 | | |
| H1 | 14 | 21 | 14 | 23 | 1 | 0.012 |
| H2 | 14 | 19 | 14 | 26 | 3 | 0.035 |
| H3 | 14 | 18 | 14 | 22 | 3 | 0.035 |
| H4 | 14 | 17 | 14 | 25 | 3 | 0.035 |
| H5 | 16 | 20 | 15 | 25 | 1 | 0.012 |
| H6 | 14 | 21 | 14 | 24 | 1 | 0.012 |
| H7 | 18 | 20 | 15 | 26 | 1 | 0.012 |
| H8 | 14 | 20 | 14 | 25 | 1 | 0.012 |
| H9 | 14 | 17 | 14 | 26 | 3 | 0.035 |
| H10 | 14 | 18 | 14 | 23 | 3 | 0.035 |
| H11 | 14 | 18 | 15 | 26 | 1 | 0.012 |
| H12 | 14 | 18 | 14 | 25 | 4 | 0.047 |
| H13 | 13 | 20 | 15 | 22 | 3 | 0.035 |
| H14 | 14 | 17 | 14 | 24 | 8 | 0.093 |
| H15 | 14 | 19 | 14 | 25 | 1 | 0.012 |
| H16 | 16 | 19 | 15 | 25 | 1 | 0.012 |
| H17 | 14 | 18 | 15 | 25 | 1 | 0.012 |
| H18 | 14 | 20 | 12 | 26 | 1 | 0.012 |
| H19 | 13 | 20 | 14 | 23 | 3 | 0.035 |
| H20 | 13 | 20 | 15 | 23 | 1 | 0.012 |
| H21 | 14 | 18 | 15 | 24 | 2 | 0.023 |
| H22 | 14 | 19 | 13 | 25 | 3 | 0.035 |
| H23 | 13 | 19 | 15 | 25 | 1 | 0.012 |
| H24 | 14 | 17 | 14 | 23 | 6 | 0.070 |
| H25 | 14 | 19 | 13 | 24 | 1 | 0.012 |
| H26 | 14 | 18 | 14 | 24 | 4 | 0.047 |
| H27 | 14 | 20 | 13 | 24 | 1 | 0.012 |
| H28 | 14 | 18 | 13 | 24 | 1 | 0.012 |
| H29 | 14 | 19 | 14 | 23 | 1 | 0.012 |
| H30 | 14 | 20 | 14 | 23 | 3 | 0.035 |
| H31 | 14 | 16 | 14 | 24 | 1 | 0.012 |
| H32 | 14 | 18 | 14 | 27 | 2 | 0.023 |
| H33 | 13 | 20 | 15 | 21 | 1 | 0.012 |
| H34 | 14 | 17 | 14 | 22 | 1 | 0.012 |
| H35 | 18 | 19 | 15 | 24 | 1 | 0.012 |
| H36 | 14 | 18 | 14 | 26 | 1 | 0.012 |
| H37 | 14 | 19 | 14 | 24 | 1 | 0.012 |
| H38 | 15 | 19 | 14 | 24 | 1 | 0.012 |
| H39 | 14 | 17 | 13 | 23 | 1 | 0.012 |
| H40 | 13 | 19 | 14 | 24 | 1 | 0.012 |
| H41 | 14 | 20 | 14 | 24 | 1 | 0.012 |
| H42 | 14 | 21 | 13 | 24 | 1 | 0.012 |
| H43 | 13 | 20 | 14 | 24 | 1 | 0.012 |
| H44 | 13 | 18 | 14 | 22 | 1 | 0.012 |
| H45 | 13 | 19 | 15 | 22 | 1 | 0.012 |
| H46 | 15 | 21 | 13 | 25 | 1 | 0.012 |
| H47 | 14 | 17 | 15 | 23 | 1 | 0.012 |
| H48 | 14 | 16 | 14 | 22 | 1 | 0.012 |
| Total | | | | | 86 | 1.000 |